

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/779,418 PB
Source: 1600 - EFS
Date Processed by STIC: 6-30-05

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IFW16

RAW SEQUENCE LISTING

DATE: 06/30/2005

PATENT APPLICATION: US/10/779,418PB

TIME: 09:50:54

Input Set : N:\efs\10779418PB_efs\4318244US-usbios-S000001.txt

Output Set: N:\CRF4\06302005\J779418PB.raw

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3 <110> APPLICANT: Bisgard-Frantzen, Henrik
4     Svendsen, Allan
5     Vedel Borchert, Torben
7 <120> TITLE OF INVENTION: METHODS FOR PRODUCING SWEETENERS AND ALCOHOL
9 <130> FILE REFERENCE: 4318.224 US
11 <140> CURRENT APPLICATION NUMBER: 10/779,418PB
12 <141> CURRENT FILING DATE: 2004-02-12
14 <150> PRIOR APPLICATION NUMBER: 10/025,648
15 <151> PRIOR FILING DATE: 2001-12-19
17 <150> PRIOR APPLICATION NUMBER: 09/902,188
18 <151> PRIOR FILING DATE: 2001-07-10
20 <150> PRIOR APPLICATION NUMBER: 09/354,191
21 <151> PRIOR FILING DATE: 1999-07-15
23 <150> PRIOR APPLICATION NUMBER: 08/600,656
24 <151> PRIOR FILING DATE: 1996-02-13
26 <150> PRIOR APPLICATION NUMBER: PCT/DK96/00056
27 <151> PRIOR FILING DATE: 1996-02-05
29 <150> PRIOR APPLICATION NUMBER: DK 0126/95
30 <151> PRIOR FILING DATE: 1995-02-03
32 <150> PRIOR APPLICATION NUMBER: DK 0336/95
33 <151> PRIOR FILING DATE: 1995-03-29
35 <150> PRIOR APPLICATION NUMBER: DK 1097/95
36 <151> PRIOR FILING DATE: 1995-09-29
38 <150> PRIOR APPLICATION NUMBER: DK 1121/95
39 <151> PRIOR FILING DATE: 1995-10-06
41 <160> NUMBER OF SEQ ID NOS: 32
43 <170> SOFTWARE: PatentIn version 3.2
45 <210> SEQ ID NO: 1
46 <211> LENGTH: 485
47 <212> TYPE: PRT
48 <213> ORGANISM: Bacillus strain NCIB 12512
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53 1           5           10           15
56 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
57           20           25           30
60 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
61           35           40           45
64 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
65           50           55           60
68 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
69 65           70           75           80
72 Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly

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76 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
77          100          105          110
80 Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
81          115          120          125
84 Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
85          130          135          140
88 Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
89 145          150          155          160
92 His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
93          165          170          175
96 Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
97          180          185          190
100 Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
101          195          200          205
104 Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
105          210          215          220
108 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
109 225          230          235          240
112 Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
113          245          250          255
116 Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
117          260          265          270
120 Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
121          275          280          285
124 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
125          290          295          300
128 Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
129 305          310          315          320
132 His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
133          325          330          335
136 Gly Glu Ala Leu Glu Ser Phe Val Gln Trp Phe Lys Pro Leu Ala
137          340          345          350
140 Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
141          355          360          365
144 Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
145          370          375          380
148 Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
149 385          390          395          400
152 Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
153          405          410          415
156 Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
157          420          425          430
160 Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
161          435          440          445
164 Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
165          450          455          460
168 Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
169 465          470          475          480

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188                               20                               25                               30
191 Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
192                               35                               40                               45
195 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
196                               50                               55                               60
199 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
200 65                               70                               75                               80
203 Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
204                               85                               90                               95
207 Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
208                               100                              105                              110
211 Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
212                               115                              120                              125
215 Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
216                               130                              135                              140
219 Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
220 145                              150                              155                              160
223 His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
224                               165                              170                              175
227 Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
228                               180                              185                              190
231 Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
232                               195                              200                              205
235 Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
236                               210                              215                              220
239 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
240 225                              230                              235                              240
243 Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
244                               245                              250                              255
247 Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
248                               260                              265                              270
251 Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
252                               275                              280                              285
255 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
256                               290                              295                              300
259 Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
260 305                              310                              315                              320
263 His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
264                               325                              330                              335

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267 Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
268           340           345           350
271 Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
272           355           360           365
275 Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
276           370           375           380
279 Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
280 385           390           395           400
283 Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
284           405           410           415
287 Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
288           420           425           430
291 Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
292           435           440           445
295 Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
296 450           455           460
299 Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
300 465           470           475           480
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304           485
307 <210> SEQ ID NO: 3
308 <211> LENGTH: 514
309 <212> TYPE: PRT
310 <213> ORGANISM: Bacillus stearothermophilus
312 <400> SEQUENCE: 3
314 Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
315 1           5           10           15
318 Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
319           20           25           30
322 Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
323           35           40           45
326 Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
327 50           55           60
330 Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr
331 65           70           75           80
334 Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
335           85           90           95
338 Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
339           100          105          110
342 Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
343           115          120          125
346 Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
347 130          135          140
350 Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
351 145          150          155          160
354 Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
355           165          170          175
358 Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
359           180          185          190

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362 Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
363      195      200      205
366 Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn
367      210      215      220
370 Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
371 225      230      235      240
374 Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly
375      245      250      255
378 Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
379      260      265      270
382 Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp
383      275      280      285
386 Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr
387      290      295      300
390 Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
391 305      310      315      320
394 Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
395      325      330      335
398 Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
399      340      345      350
402 Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
403      355      360      365
406 Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
407      370      375      380
410 Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
411 385      390      395      400
414 Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val
415      405      410      415
418 Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
419      420      425      430
422 Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
423      435      440      445
426 Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
427      450      455      460
430 Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
431 465      470      475      480
434 Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Ser Ile Thr Thr
435      485      490      495
438 Arg Pro Trp Thr Asp Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
439      500      505      510
442 Ala Trp
446 <210> SEQ ID NO: 4
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448 <212> TYPE: DNA
449 <213> ORGANISM: Bacillus strain NCIB 12512
451 <400> SEQUENCE: 4
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454 gggaatcatt ggaacagggt gagggatgac gcagctaact taaagagtaa agggataaca      120
456 gctgtatgga tcccacctgc atggaagggg acttcccaga atgatgtagg ttatggagcc      180

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32

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